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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=20; hr=15; min=6; sec=9; ms=551; ]

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Application No: 10547447 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2008-02-29 16:55:52.428  
**Finished:** 2008-02-29 16:55:58.398  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 970 ms  
**Total Warnings:** 41  
**Total Errors:** 35  
**No. of SeqIDs Defined:** 59  
**Actual SeqID Count:** 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)

**Input Set:**

**Output Set:**

**Started:** 2008-02-29 16:55:52.428  
**Finished:** 2008-02-29 16:55:58.398  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 970 ms  
**Total Warnings:** 41  
**Total Errors:** 35  
**No. of SeqIDs Defined:** 59  
**Actual SeqID Count:** 59

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (28)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (31)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)

**Input Set:**

**Output Set:**

**Started:** 2008-02-29 16:55:52.428  
**Finished:** 2008-02-29 16:55:58.398  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 970 ms  
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**Total Errors:** 35  
**No. of SeqIDs Defined:** 59  
**Actual SeqID Count:** 59

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (40)
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W 213	Artificial or Unknown found in <213> in SEQ ID (41)
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W 213	Artificial or Unknown found in <213> in SEQ ID (44) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (44) This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> Renz, Andreas  
Heinz, Ernst  
Abbadì, Amine  
Domergue, Frederic  
Zank, Thorsten

<120> METHOD FOR THE PRODUCTION OF POLYUNSATURATED FATTY ACIDS

<130> 12810-00119-US

<140> 10547447

<141> 2005-08-26

<150> PCT/EP2004/000771

<151> 2001-01-29

<150> DE 103 08 836.9

<151> 2003-02-27

<160> 59

<170> PatentIn version 3.5

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<211> 849

<212> DNA

<213> Caenorhabditis elegans

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<221> CDS

<222> (1)..(849)

<223> Acyl-CoA:lysophospholipid acyltransferase

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Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile

20 25 30

tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144

Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val

35 40 45

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Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe

50 55 60

cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val

65 70 75 80

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Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys	
85 90 95	
aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg	336
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro	
100 105 110	
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc	384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe	
115 120 125	
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat	432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr	
130 135 140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg	480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met	
145 150 155 160	
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat	528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn	
165 170 175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca	576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala	
180 185 190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg	624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg	
195 200 205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt	672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val	
210 215 220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat	720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp	
225 230 235 240	
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Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala	
245 250 255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt	816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg	
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<213> Caenorhabditis elegans

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Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val  
35 40 45

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe  
50 55 60

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val  
65 70 75 80

Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys  
85 90 95

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro  
100 105 110

Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe  
115 120 125

Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr  
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Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn  
165 170 175

Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala  
180 185 190

Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg  
195 200 205

Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val  
 210 215 220

Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp  
 225 230 235 240

Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala  
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Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu  
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<210> 3  
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 <212> DNA  
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 <221> CDS  
 <222> (1)..(849)  
 <223> Acyl-CoA:lysophospholipid acyltransferase

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 Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile  
 20 25 30  
 tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144  
 Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val  
 35 40 45  
 aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt 192  
 Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe  
 50 55 60  
 cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240  
 His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val  
 65 70 75 80  
 tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt 288  
 Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys  
 85 90 95  
 aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg 336



Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro	
100 105 110	
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc	384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe	
115 120 125	
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat	432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr	
130 135 140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg	480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met	
145 150 155 160	
aag aac aga aat ctt aaa ctt tgg gta tct ccg gaa gga aca aga aat	528
Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn	
165 170 175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca	576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala	
180 185 190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg	624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg	
195 200 205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt	672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val	
210 215 220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat	720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp	
225 230 235 240	
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc	768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala	
245 250 255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt	816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg	
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gga gaa aca aaa gac ggg aag aaa tct gag taa	849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu	
275 280	

<210> 4  
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 <212> PRT  
 <213> Caenorhabditis elegans

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Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
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Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile  
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Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val  
35 40 45

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe  
50 55 60

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val  
65 70 75 80

Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys  
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Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro  
100 105 110

Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe  
115 120 125

Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr  
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Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met  
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Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala  
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Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg  
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Phe	Ile	Leu	Tyr	Asn	Ile	Ser	Thr	Val	Cys	His	Tyr	Tyr	Val	Arg	Ile	
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tcg	ttt	tat	tac	ttc	aca	att	tta	ttg	cat	gga	atg	gaa	gtt	tgt	gtt	144
Ser	Phe	Tyr	Tyr	Phe	Thr	Ile	Leu	Leu	His	Gly	Met	Glu	Val	Cys	Val	
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Thr	Met	Ile	Pro	Ser	Trp	Leu	Asn	Gly	Lys	Gly	Ala	Asp	Tyr	Val	Phe	
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Tyr	Gly	Tyr	Glu	Lys	Thr	Gln	Val	Glu	Gly	Pro	Ala	Val	Val	Ile	Cys	
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Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala	
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gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg	624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg	
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Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg	
260 265 270	
gga gaa aca aaa gac ggg aag aaa tct gag taa	